

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:
Matt Sauer et al.

Application No.: 10/524,827

Confirmation No.: 1457

Filed: February 18, 2005

Art Unit: 1633

For: PROCESS FOR PREPARING
KETOCAROTENOIDS IN GENETICALLY
MODIFIED ORGANISMS

Examiner: Kevin K. Hill

AMENDMENT AND RESPONSE TO RESTRICTION REQUIREMENT

MS Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

INTRODUCTORY COMMENTS

In response to the Office Communication dated April 4, 2006, please amend the above-identified U.S. patent application as follows:

Amendments to the Claims are reflected in the listing of claims which begins on page 2 of this paper.

Remarks/Arguments begin on page 11 of this paper.

AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A process for preparing ketocarotenoids by cultivating genetically modified organisms which, compared with the wild type, have a modified ketolase activity, and the modified ketolase activity is caused by a ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2.
2. (Currently amended) A The process as claimed in claim 1, wherein organisms which, as wild type, already have a ketolase activity, and the genetic modification brings about an increase in the ketolase activity compared with the wild type, are used.
3. (Currently amended) A The process as claimed in claim 1, wherein the ketolase activity is increased by increasing the gene expression of a nucleic acid encoding a ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2, compared with the wild type.
4. (Currently amended) A The process as claimed in claim 3, wherein the gene expression is increased by introducing nucleic acids which encode ketolases comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2, compared with the wild type, into the organism.
5. (Currently amended) A The process as claimed in claim 1, wherein organisms which, as wild type, have no ketolase activity are used, and the genetic modification causes a ketolase activity compared with the wild type.

6. (Currently amended) A The process as claimed in claim 5, wherein genetically modified organisms which transgenically express a ketolase comprising the amino acid sequence ~~SEQ ID NO: 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ ID NO: 2~~ SEQ ID NO: 2, are used.
7. (Currently amended) A The process as claimed in claim 5, wherein the gene expression is caused by introducing nucleic acids which encode ketolases comprising the amino acid sequence ~~SEQ ID NO: 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ ID NO: 2~~ SEQ ID NO: 2, into the organism.
8. (Currently amended) A The process as claimed in claim 5, wherein nucleic acids comprising the sequence ~~SEQ ID NO: 1~~ SEQ ID NO: 1 are introduced.
9. (Currently amended) A The process as claimed in claim 1, wherein the organisms additionally have an increased activity, compared with the wild type, of at least one of the activities selected from the group of hydroxylase activity and β -cyclase activity.
10. (Currently amended) A The process as claimed in claim 9, wherein the gene expression of at least one nucleic acid selected from the group of nucleic acids encoding a hydroxylase, and nucleic acids encoding a β -cyclase, is increased compared with the wild type for the additional increase in at least one of the activities.
11. (Currently amended) A The process as claimed in claim 10, wherein the gene expression is increased by introducing at least one nucleic acid selected from the group of nucleic acids encoding a hydroxylase and nucleic acids encoding a β -cyclase into the organism.
12. (Currently amended) A The process as claimed in claim 11, wherein nucleic acids which encode a hydroxylase comprising the amino acid sequence SEQ ID NO: 16 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has

an identity of at least 20% at the amino acid level with the sequence SEQ ID NO: 16 are introduced as nucleic acid encoding a hydroxylase.

13. (Currently amended) A The process as claimed in claim 12, wherein nucleic acids comprising the sequence SEQ ID NO: 15 are introduced.

14. (Currently amended) A The process as claimed in claim 11, wherein nucleic acids which encode a β -cyclase comprising the amino acid sequence SEQ ID NO: 18 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 20% at the amino acid level with the sequence SEQ ID NO: 18 are introduced as nucleic acid encoding a β -cyclase.

15. (Currently amended) A The process as claimed in claim 14, wherein nucleic acids comprising the sequence SEQ ID NO: 17 are introduced.

16. (Currently amended) A The process as claimed in claim 1, wherein the genetically modified organisms are harvested after cultivation, and subsequently the ketocarotenoids are isolated from the organisms.

17. (Currently amended) A The process as claimed in claim 1, wherein an organism which is able as starting organism naturally or through genetic complementation or reregulation of metabolic pathways to produce carotenoids is used as organism.

18. (Currently amended) A The process as claimed in claim 1, wherein microorganisms or plants are used as organisms.

19. (Currently amended) A The process as claimed in claim 18, wherein bacteria, yeasts, algae or fungi are used as microorganisms.

20. (Currently amended) A The process as claimed in claim 19, wherein the microorganisms are selected from the group of *Escherichia*, *Erwinia*, *Agrobacterium*, *Flavobacterium*,

Alcaligenes, Paracoccus, Nostoc, cyanobacteria of the genus *Synechocystis*, *Candida*, *Saccharomyces*, *Hansenula*, *Phaffia*, *Pichia*, *Aspergillus*, *Trichoderma*, *Ashbya*, *Neurospora*, *Blakeslea*, *Phycomyces*, *Fusarium*, *Haematococcus*, *Phaedactylum tricornatum*, *Volvox* or *Dunaliella*.

21. (Currently amended) A The process as claimed in claim 18, wherein plants are used as organism.

22. (Currently amended) A The process as claimed in claim 21, wherein a plant selected from the families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassicaceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Illiaceae or Lamiaceae is used as plant.

23. (Currently amended) A The process as claimed in claim 22, wherein a plant selected from the plant genera Marigold, Tagetes erecta, Tagetes patula, Acacia, Aconitum, Adonis, Arnica, Aquilegia, Aster, Astragalus, Bignonia, Calendula, Caltha, Campanula, Canna, Centaurea, Cheiranthus, Chrysanthemum, Citrus, Crepis, Crocus, Curcubita, Cytisus, Delonia, Delphinium, Dianthus, Dimorphotheca, Doronicum, Eschscholtzia, Forsythia, Fremontia, Gazania, Gelsemium, Genista, Gentiana, Geranium, Gerbera, Geum, Grevillea, Helenium, Helianthus, Hepatica, Heracleum, Hibiscus, Heliopsis, Hypericum, Hypochoeris, Impatiens, Iris, Jacaranda, Kerria, Laburnum, Lathyrus, Leontodon, Lilium, Linum, Lotus, Lycopersicon, Lysimachia, Maratia, Medicago, Mimulus, Narcissus, Oenothera, Osmanthus, Petunia, Photinia, Physalis, Phyteuma, Potentilla, Pyracantha, Ranunculus, Rhododendron, Rosa, Rudbeckia, Senecio, Silene, Silphium, Sinapsis, Sorbus, Spartium, Tecoma, Torenia, Tragopogon, Trollius, Tropaeolum, Tulipa, Tussilago, Ulex, Viola or Zinnia is used as plant.

24. (Currently amended) A The process as claimed in claim 1, wherein the ketocarotenoids are selected from the group of astaxanthin, canthaxanthin, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, adonirubin and adonixanthin.

25. (Currently amended) A genetically modified organism where the genetic modification

- (a) in the case where the wild-type organism already has a ketolase activity, increases the activity of a ketolase compared with the wild type and
- (b) in the case where the wild-type organism has no ketolase activity, causes the activity of a ketolase compared with the wild type,

and the ketolase activity which has been increased as in (a) or caused as in (b) is caused by a ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2.

26. (Currently amended) A The genetically modified organism as claimed in claim 25, wherein the increasing or causing of the ketolase activity is brought about by an increasing or causing of the gene expression of a nucleic acid encoding a ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2, compared with the wild type.

27. (Currently amended) A The genetically modified organism as claimed in claim 26, wherein to increase or cause the gene expression nucleic acids which encode ketolases comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2, are introduced into the organism.

28. (Currently amended) A genetically modified organism comprising at least one transgenic nucleic acid encoding a ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ. ID. NO. 2~~ SEQ ID NO: 2.

29. (Currently amended) A genetically modified organism comprising at least two endogenous nucleic acids encoding a ketolase comprising the amino acid sequence ~~SEQ ID NO: 2~~ SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% at the amino acid level with the sequence ~~SEQ ID NO: 2~~ SEQ ID NO: 2.
30. (Currently amended) A The genetically modified organism as claimed in claim 25, wherein the genetic modification additionally increases at least one of the activities selected from the group of hydroxylase activity and β -cyclase activity, compared with the wild type.
31. (Currently amended) A The genetically modified organism as claimed in claim 25, which is able as starting organism naturally or through genetic complementation to produce carotenoids.
32. (Currently amended) A The genetically modified organism as claimed in claim 25, selected from the group of microorganisms or plants.
33. (Currently amended) A The genetically modified organism as claimed in claim 32, wherein the microorganisms are selected from the group of bacteria, yeasts, algae or fungi.
34. (Currently amended) A The genetically modified microorganism as claimed in claim 33, wherein the microorganisms are selected from the group of *Escherichia*, *Erwinia*, *Agrobacterium*, *Flavobacterium*, *Alcaligenes*, *Paracoccus*, *Nostoc*, cyanobacteria of the genus *Synechocystis*, *Candida*, *Saccharomyces*, *Hansenula*, *Pichia*, *Aspergillus*, *Trichoderma*, *Ashbya*, *Neurospora*, *Blakeslea*, *Phycomyces*, *Fusarium*, *Haematococcus*, *Phaedactylum tricornatum*, *Volvox* or *Dunaliella*.
35. (Currently amended) A The genetically modified plant as claimed in claim 32, wherein the plants are selected from the families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassiceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae,

Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Iliiaceae or Lamiaceae.

36. (Currently amended) A The genetically modified plant as claimed in claim 35, wherein the plants are selected from the plant genera Marigold, Tagetes erecta, Tagetes patula, Acacia, Aconitum, Adonis, Arnica, Aquilegia, Aster, Astragalus, Bignonia, Calendula, Caltha, Campanula, Canna, Centaurea, Cheiranthus, Chrysanthemum, Citrus, Crepis, Crocus, Curcubita, Cytisus, Delonia, Delphinium, Dianthus, Dimorphotheca, Doronicum, Eschscholtzia, Forsythia, Fremontia, Gazania, Gelsemium, Genista, Gentiana, Geranium, Gerbera, Geum, Grevillea, Helenium, Helianthus, Hepatica, Heracleum, Hibiscus, Heliopsis, Hypericum, Hypochoeris, Impatiens, Iris, Jacaranda, Kerria, Laburnum, Lathyrus, Leontodon, Lilium, Linum, Lotus, Lycopersicon, Lysimachia, Maratia, Medicago, Mimulus, Narcissus, Oenothera, Osmanthus, Petunia, Photinia, Physalis, Phyteuma, Potentilla, Pyracantha, Ranunculus, Rhododendron, Rosa, Rudbeckia, Senecio, Silene, Silphium, Sinapsis, Sorbus, Spartium, Tecoma, Torenia, Tragopogon, Trollius, Tropaeolum, Tulipa, Tussilago, Ulex, Viola or Zinnia.

37. (Previously presented) The genetically modified organisms as claimed in claim 25, where the organism is used as animal or human food.

38. (Previously presented) The genetically modified organisms as claimed in claim 25, where the organism produces ketocarotenoid-containing extracts or animal and human food supplements.

39. (Currently amended) A ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 8~~ SEQ ID NO: 8 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence ~~SEQ. ID. NO. 8~~ SEQ ID NO: 8, with the proviso that the amino acid sequence ~~SEQ. ID NO. 4~~ SEQ ID NO: 4 is not present.

40. (Currently amended) A ketolase comprising the amino acid sequence ~~SEQ. ID. NO. 6~~ SEQ ID NO: 6 or a sequence which is derived from this sequence by substitution, insertion or

deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence ~~SEQ ID NO: 6~~ SEQ ID NO: 6.

41. (Currently amended) A ketolase comprising the amino acid sequence ~~SEQ ID NO: 12~~ SEQ ID NO: 12 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence ~~SEQ ID NO: 12~~ SEQ ID NO: 12, with the proviso that the amino acid sequence ~~SEQ ID NO: 6~~ SEQ ID NO: 6 is not present.

42. (Currently amended) A ketolase comprising the amino acid sequence ~~SEQ ID NO: 49~~ SEQ ID NO: 49 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 50% at the amino acid level with the sequence ~~SEQ ID NO: 49~~ SEQ ID NO: 49, with the proviso that the amino acid sequence ~~SEQ ID NO: 47~~ SEQ ID NO: 47 is not present.

43. (Previously presented) A nucleic acid encoding a protein as claimed in claim 39, with the proviso that the sequence SEQ ID NO: 5 is not present.

44. (Currently amended) A protein comprising the amino acid sequence ~~SEQ ID NO: 4~~ SEQ ID NO: 4 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence ~~SEQ ID NO: 4~~ SEQ ID NO: 4, and which has the property of a ketolase.

45. (Currently amended) A protein comprising the amino acid sequence ~~SEQ ID NO: 6~~ SEQ ID NO: 6 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 65% at the amino acid level with the sequence ~~SEQ ID NO: 6~~ SEQ ID NO: 6, and which has the property of a ketolase.

46. (Currently amended) A protein comprising the amino acid sequence ~~SEQ ID NO: 47~~ SEQ ID NO: 47 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 50% at the amino acid level with the

sequence ~~SEQ ID NO: 47~~ SEQ ID NO: 47 and which has the property of a ketolase.

47. (New) The process as claimed in claim 22, wherein the plant is a plant from the family Asteraceae.

48. (New) The process as claimed in claim 23, wherein the plant is *Tageta erecta*.

49. (New) The process as claimed in claim 3, wherein the nucleic acid encoding a ketolase comprises the amino acid sequence of SEQ ID NO: 2.

50. (New) The process as claimed in claim 4, wherein the nucleic acids which encode ketolases comprise the amino acid sequence of SEQ ID NO: 2.

51. (New) The process as claimed in claim 12, wherein the nucleic acids which encode a hydroxylase comprise the amino acid sequence SEQ ID NO: 16.

52. (New) The process as claimed in claim 14, wherein the nucleic acids which encode a β -cyclase comprise the amino acid sequence SEQ ID NO: 18.

REMARKS

Claims 1-52 are pending. Claims 1-36, 39-42 and 44-46 have been amended to better comply with U.S. practice. Claims 47-52 have been added and find support in original claims 3, 4, 12, 14, 22 and 23. No new matter has been added. It is believed that new claims 47-52 correspond to Group I.

Provisional Election

In response to the restriction requirement set forth in the Office Action mailed April 4, 2006, Applicants hereby provisionally elect Group I, claims 1-38 which additionally encompasses new claims 47-52; a ketolase comprising the amino acid sequence of SEQ ID NO: 2 (claims 1-38, 47-52); a hydroxylase comprising the amino acid sequence of SEQ ID NO: 16 (claims 9-13, 30, 51); a β -cyclase comprising the amino acid sequence of SEQ ID NO: 18 (claims 9-11, 14, 15, 30, 52); a plant (claims 1-18, 21-32, 35-38, 47, 48); a plant from the plant family Asteraceae (claims 1-18, 21-32, 35-38, 47, 48); a plant from *Tagetes erecta* (claims 1-18, 21-32, 35-38, 47, 48); the species "wherein the organism, as wildtype, has no ketolase activity" (claims 1, 3-38, 47-52); and the species "(i) genetically modified with ketolase (a), comprising the amino acid sequence SEQ ID NO:2" (claims 1-38, 47-52), with traverse. Applicants urge reconsideration of the restriction requirement for the reasons below.

The Claims of Groups I-IV Share The Same Or Corresponding Special Technical Feature.

The Examiner has required restriction between Groups I to IV. The Examiner stated that the linking technical feature of the present invention is "an organism genetically modified with a nucleotide functionally encoding a ketolase comprising the amino acid sequence of SEQ ID NO: 2." (Office Action, page 3). The Examiner has alleged that this technical feature does not constitute a contribution over the prior art. No prior art, however has been cited, nor has any argument been presented in support of this statement. Thus, the PTO has failed to make a *prima facie* case of lack of unity between Groups I-IV. Reconsideration and removal of the restriction requirement is respectfully urged.

The Claims Of Group I Share The Same Or Corresponding Special Technical Feature.

Because this application is a national stage filing pursuant to 35 U.S.C. § 371, unity of invention under PCT Rule 13.1 and 13.2 is the applicable standard. Unity of invention is fulfilled “when there is a technical relationship among those inventions involving one or more of the same or corresponding special technical feature. The expression ‘special technical feature’ shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, makes over the prior art.” (PCT Rule 13.2).

The Examiner has required additional restrictions if Group I is elected.

Claims 1-38 of Group I relate to a process for preparing ketocarotenoids by cultivating genetically modified organisms having modified ketolase activity caused by a ketolase comprising the amino acid sequence of SEQ ID NO: 2 or a derivative thereof and to a genetically modified organism having modified ketolase activity caused by a ketolase comprising the amino acid sequence of SEQ ID NO: 2 or a derivative thereof.

Thus, claims 1-38 in Group I share the “special technical feature” of a modified ketolase activity caused by a ketolase comprising the amino acid sequence of SEQ ID NO: 2 or a derivative thereof. This is the “single general inventive concept” of the present invention as required under PCT Rule 13. Although the Examiner has asserted this is not inventive, no support is given for this assertion.

The Examiner has required that if Applicants elect Group I, an additional election to a single ketolase must be made, for example as seen in claim 1. The Examiner acknowledges that the ketolases recited in claims 1, 3-4, 6-7 and 25-29 have a common structure in that they comprise the amino acid sequence of SEQ ID NO: 2. However, the Examiner alleges that the ketolases are not regarded as being similar in nature because all the alternatives do not share a common property or activity.

Applicants respectfully disagree. Claim 1 recites that the genetically modified organisms have a “modified ketolase activity” which is “caused by a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence.” Thus, claim 1

recites that the sequences are ketolases and have ketolase activity. Thus, the alternatives of claim 1 have a common structure, as acknowledged by the Examiner, and additionally share a common activity. Furthermore, the modified ketolase activity recited in the claims is an understood activity to the skilled person. A ketolase has the enzymatic activity of introducing a keto group on the β -ionone ring of carotenoids, and particularly of converting β -carotene into canthaxanthin. (Specification, page 3, lines 15-19). Thus, the ketolases encompassed by claim 1 share a structure and activity. For these reasons, the requirement of a technical interrelationship and the same or corresponding special technical features as defined under Rule 13.2 is met. (see Chapter 10 § 10.17 of the PCT International Search and Preliminary Examination Guidelines established by the International Bureau of WIPO for the determination of Unity of Invention, applicable to national stage applications under 35 U.S.C. § 371).

Unity Of Invention Must Be Considered First Only In Relation To Independent Claims.

The Examiner has further required that if Applicants elect Group I, additional elections to a single hydroxylase, a single β -cyclase, and a single organism must be made. In addition, the Examiner has also required that if Group I and a microorganism is elected, then a further election to a single microorganism be made as recited in dependent claims 20 and 34. Likewise, the Examiner has additionally required that if Group I and a plant is elected, then a further election to a single plant family as recited in dependent claims 22 and 35 must be made. The Examiner has additionally required that if Group I and a plant family is elected then a further election to a single plant genus as recited in dependent claims 23 and 36 must be made. The Examiner also stated that these were group restrictions and should not be construed as election of species.

PCT Rules 13.1 and 13.2, as explained in Chapter 10 of the PCT International Search and Preliminary Examination Guidelines, are the applicable standard for determining unity of invention during the national stage of an international application under 35 U.S.C. § 371. See also MPEP § 1850. Please note that in Chapter 10 §10.06 of these Guidelines, unity of invention must be “considered in the first place only in relation to the independent claims” and not the dependent claims. Furthermore, Chapter 10 §10.07 of the Guidelines states that “[i]f the independent claims avoid the prior art and satisfy the requirement of unity of invention, no

problem of lack of unity arises in respect to any claims that depend on the independent claims. In particular, it does not matter if a dependent claim itself contains a further invention.”

The claims drawn to a single hydroxylase, a single β -cyclase, a single organism, and further to a single microorganism, plant, plant family and plant genus, exemplified in claims 12, 14, 20, 22, 23, and 34-36, all depend indirectly or directly from claim 1 or from claim 25 which incorporates the special technical feature of claim 1. The Examiner has inappropriately required elections based on dependent claims. Furthermore, the Patent Office has not established that independent claim 1 or 25 does not avoid the prior art since no prior art has been cited. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the restriction requirement within Group I and examine all the claims of at least Group I in one application.

An Election Of Species Recited In Dependent Claims Is Inappropriate.

The Examiner has additionally required elections of species if the Applicants elect Group I and an organism.

First, the Examiner has required a species election based on whether or not the organism as a wild type has ketolase activity. The Examiner stated that claim 2, 5, 16-17, 25-27 and 30-31 are generic. Independent claim 25 and dependent claims 2 and 5 are the claims that recite the features described by the Examiner as requiring an election of species. With respect to dependent claims 2 and 5 and the claims dependent therefrom, and the claims dependent from claim 25, the Examiner has asserted a lack of unity of invention necessitating an election of species based on dependent claims. As explained above, unity of invention must be considered in the first place in relation only to independent claims. Furthermore, the Examiner states that the technical feature linking the members is “an organism.” Applicants respectfully disagree. The Examiner has asserted a different technical feature for this restriction than for the restriction to Groups I-IV or for the second species restriction discussed below. Independent claim 25, all the generic claims, and the claims dependent therefrom all share the same or corresponding technical feature of “ketolase activity caused by a ketolase comprising the amino acid sequence of SEQ ID NO: 2” and a derivative thereof. Moreover, the special technical feature of “ketolase

activity caused by a ketolase comprising the amino acid sequence of SEQ ID NO: 2” and a derivative thereof as recited in independent claim 1 and 25 is shared by all the claims of Group I including dependent claims 2 and 5 and the claims dependent therefrom and the claims dependent on claim 25.

Second, the Examiner has required an election of one species of genetically modified organisms recited in claims 1-15, 17 and 25-31 and stated that these claims were generic. Even though for this species election the technical feature linking the members is described as “a polypeptide comprising the amino acid sequence of SEQ ID NO: 2” the Examiner nevertheless alleges that each of the species does not share a substantially common structural feature or function because they are drawn to multiple organisms that are structurally, genetically and physiological distinct. The technical feature asserted by the Examiner has not been applied to determine unity for this second species restriction. The Patent Office has not established why the technical feature asserted as linking the members for the second species restriction that of “a polypeptide comprising the amino acid sequence of SEQ ID NO: 2” does not constitute a common structural feature or function. As mentioned above the special technical feature of “ketolase activity caused by a ketolase comprising the amino acid sequence of SEQ ID NO: 2” or a derivative thereof as recited in independent claim 1 and 25 is shared by all the claims of Group I. Because the claims of Group I either depend directly or indirectly from claim 1 or claim 25 which incorporates the technical feature of claim 1, all the claims of Group I share the same or a corresponding technical feature. Thus, unity of invention is fulfilled pursuant to 37 CFR § 1.475 for all the claims of Group I.

The Examiner also stated that the inventions are distinct because they have acquired separate status in the art because of their divergent subject matter and the requirement for different searches which would impose a serious search burden. Please note that in Chapter 10 §10.05 of the PCT International Search and Preliminary Examination Guidelines, an objection of lack of unity of invention should not be raised merely “because the inventions claimed are classified in separate classification groups or merely for the purpose of restricting the international search to certain classification groups.”

The International Examiner Found Unity Of Invention Regarding The Claims of Group I.

Furthermore, the International Search Authority and the International Examination Authority, as shown in the International Search Report and the International Preliminary Examination Report, has not found a lack of unity of invention for the claims of Group I when applying PCT Rules 13.1 and 13.2, suggesting unity within this group.

Additionally, Applicants believe that there is no undue burden on the Examiner to search and examine all the claims of Group I. As previously noted, this is a 371 application from a PCT application, and all the claims of Group I (claims 1-38) were searched by the International Search Authority and the International Examination Authority. A search directed to ketolase comprising the amino acid sequence of SEQ ID NO: 2 would overlap with a search of organisms containing these sequences and thus there is no undue burden if considered together.

Applicants respectfully submit that the restriction requirement within Group I should be withdrawn even under restriction practice. As stated in § 803 of the M.P.E.P. “[i]f the search and examination of the entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to independent or distinct inventions.” (M.P.E.P. § 803, emphasis added). Since the search has already been conducted for all the claims of Group I by the International Search Authority and the International Examination Authority, there would be no undue burden on the Examiner to examine at least the claims of Group I together.

Conclusion

For at least the above reasons, Applicants respectfully request that the restriction requirement be reconsidered and withdrawn and that all the claims be examined in one application, or at least the claims of Group I be examined in one application.

Accompanying this response is a petition for a one month extension of time to and including June 4, 2006 to respond to the Office Action mailed April 4, 2005 with the required fee authorization. A fee sheet authorizing payment for the new claims is also enclosed. No further fee is believed due. However, if an additional fee is due, the Director is authorized to charge our

Deposit Account No. 03-2775, under Order No. 13173-00006-US from which the undersigned is authorized to draw.

Respectfully submitted,

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